CLAIMS

1. A method for detecting the genotype in a nucleic acid sample, comprising the following step (a):

(a) analyzing two or more polymorphisms selected from the group consisting of the following (1) to (6) in a nucleic acid sample:

(1) polymorphism at the base number position 3932 of the apolipoprotein E gene;

(2) polymorphism at the base number position 1648 of the glycoprotein Ia gene;

(3) polymorphism at the base number position -863 of the tumor necrosis factor-α gene;

(4) polymorphism at the base number position 825 of G-protein β3 subunit gene;

(5) polymorphism at the base number position -482 of the apolipoprotein C-III gene; and

(6) polymorphism at the base number position -6 of the angiotensinogen gene.

2. A method for detecting the genotype in a nucleic acid sample, comprising the following step (b):

(b) analyzing two or more polymorphisms selected from the group consisting of the following (7) to (11) in a nucleic acid sample:

(7) polymorphism at the base number position 1186 of the thrombospondin 4 gene;

(8) polymorphism at the base number position -863 of the tumor necrosis factor-α gene;

(9) polymorphism at the base number position 2136 of the thrombomodulin gene;

(10) polymorphism at the base number position 5713 of the thrombopoietin gene; and

(11) polymorphism at the base number position 994 of the platelet-activating factor acetylhydrolase gene.

3. A method for detecting the genotype in a nucleic acid sample, comprising

the following step (c):

(c) analyzing two or more polymorphisms selected from the group consisting of the following (12) to (17) in a nucleic acid sample:

(12) polymorphism at the base number position 561 of the E-selectin gene;

(13) polymorphism at the base number position 2445 of the fatty acid-binding protein 2 gene;

(14) polymorphism at the base number position 1018 of the glycoprotein Ibα gene;

(15) polymorphism at the base number position -668 of the plasminogen activator inhibitor-1 gene;

(16) polymorphism at the base number position 584 of the paraoxonase gene; and

(17) polymorphism at the base number position 3932 of the apolipoprotein E gene.

4. A method for detecting the genotype in a nucleic acid sample, comprising the following step (d):

(d) analyzing two or more polymorphisms selected from the group consisting of the following (18) to (22) in a nucleic acid sample:

(18) polymorphism at the base number position -668 of the plasminogen activator inhibitor-1 gene;

(19) polymorphism at the base number position -482 of the apolipoprotein C-III gene;

(20) polymorphism at the base number position 584 of the paraoxonase gene;

(21) polymorphism at the base number position 1018 of glycoprotein Ibα gene; and

(22) polymorphism at the base number position 3932 of the apolipoprotein E gene.

5. A method for diagnosing the risk of restenosis after coronary angioplasty, comprising the following steps (i) to (iii):

(i) analyzing two or more polymorphisms selected from the group consisting of the following (1) to (6) in a nucleic acid sample;

(1) polymorphism at the base number position 3932 of the apolipoprotein E gene;

(2) polymorphism at the base number position 1648 of the glycoprotein Ia gene;

(3) polymorphism at the base number position -863 of the tumor necrosis factor-α gene;

(4) polymorphism at the base number position 825 of G-protein β3 subunit gene;

(5) polymorphism at the base number position -482 of the apolipoprotein C-III gene; and

(6) polymorphism at the base number position -6 of the angiotensinogen gene;

(ii) determining, based on the information about polymorphism which was obtained in the step (i), the genotype of the nucleic acid sample; and

(iii) assessing, based on the genotype determined, a genetic risk of restenosis after coronary angioplasty.

6. A method for diagnosing the risk of restenosis after coronary angioplasty, comprising the following steps (iv) to (vi):

(iv) analyzing two or more polymorphisms selected from the group consisting of the following (7) to (11) in a nucleic acid sample;

(7) polymorphism at the base number position 1186 of the thrombospondin 4 gene;

(8) polymorphism at the base number position -863 of the tumor necrosis factor-α gene;

(9) polymorphism at the base number position 2136 of the thrombomodulin gene;

(10) polymorphism at the base number position 5713 of the thrombopoietin gene; and

(11) polymorphism at the base number position 994 of the platelet-activating factor acetylhydrolase gene;

(v) determining, based on the information about polymorphism which was obtained in the step (iv), the genotype of the nucleic acid sample; and

(vi) assessing, based on the genotype determined, a genetic risk of restenosis after coronary angioplasty.

7. A method for diagnosing the risk of restenosis after coronary angioplasty, comprising the following steps (vii) to (ix):

(vii) analyzing two or more polymorphisms selected from the group consisting of the following (12) to (17) in a nucleic acid sample;

(12) polymorphism at the base number position 561 of the E-selectin gene;

(13) polymorphism at the base number position 2445 of the fatty acid-binding protein 2 gene;

(14) polymorphism at the base number position 1018 of the glycoprotein Ibα gene;

(15) polymorphism at the base number position -668 of the plasminogen activator inhibitor-1 gene;

(16) polymorphism at the base number position 584 of the paraoxonase gene; and

(17) polymorphism at the base number position 3932 of the apolipoprotein E gene;

(viii) determining, based on the information about polymorphism which was obtained in the step (vii), the genotype of the nucleic acid sample; and

(ix) assessing, based on the genotype determined, a genetic risk of restenosis after coronary angioplasty.

8. A method for diagnosing the risk of restenosis after coronary angioplasty, comprising the following steps (x) to (xii):

(x) analyzing two or more polymorphisms selected from the group consisting of the following (18) to (22) in a nucleic acid sample;

(18) polymorphism at the base number position -668 of the plasminogen activator inhibitor-1 gene;

(19) polymorphism at the base number position -482 of the apolipoprotein C-III gene;

(20) polymorphism at the base number position 584 of the paraoxonase gene;

(21) polymorphism at the base number position 1018 of glycoprotein Ibα gene; and

(22) polymorphism at the base number position 3932 of the

apolipoprotein E gene;

(xi) determining, based on the information about polymorphism which was obtained in the step (x), the genotype of the nucleic acid sample; and

(xii) assessing, based on the genotype determined, a genetic risk of restenosis after coronary angioplasty.

9. A kit for detecting the genotype, comprising two or more of nucleic acids selected from the group consisting of the following (1) to (6):

(1) a nucleic acid for analyzing polymorphism at the base number position 3932 of the apolipoprotein E gene;

(2) a nucleic acid for analyzing polymorphism at the base number position 1648 of the glycoprotein Ia gene;

(3) a nucleic acid for analyzing polymorphism at the base number position -863 of the tumor necrosis factor-α gene;

(4) a nucleic acid for analyzing polymorphism at the base number position 825 of G-protein β3 subunit gene;

(5) a nucleic acid for analyzing polymorphism at the base number position -482 of the apolipoprotein C-III gene; and

(6) a nucleic acid for analyzing polymorphism at the base number position -6 of the angiotensinogen gene.

10. A kit for detecting the genotype, comprising two or more of nucleic acids selected from the group consisting of the following (7) to (11):

(7) a nucleic acid for analyzing polymorphism at the base number position 1186 of the thrombospondin 4 gene;

(8) a nucleic acid for analyzing polymorphism at the base number position -863 of the tumor necrosis factor-α gene;

(9) a nucleic acid for analyzing polymorphism at the base number position 2136 of the thrombomodulin gene;

(10) a nucleic acid for analyzing polymorphism at the base number position 5713 of the thrombopoietin gene; and

(11) a nucleic acid for analyzing polymorphism at the base number position 994 of the platelet-activating factor acetylhydrolase gene.

11. A kit for detecting the genotype, comprising two or more of nucleic acids

selected from the group consisting of the following (12) to (17):

(12) a nucleic acid for analyzing polymorphism at the base number position 561 of the E-selectin gene;

(13) a nucleic acid for analyzing polymorphism at the base number position 2445 of the fatty acid-binding protein 2 gene;

(14) a nucleic acid for analyzing polymorphism at the base number position 1018 of glycoprotein Ibα gene;

(15) a nucleic acid for analyzing polymorphism at the base number position -668 of the plasminogen activator inhibitor-1 gene;

(16) a nucleic acid for analyzing polymorphism at the base number position 584 of the paraoxonase gene; and

(17) a nucleic acid for analyzing polymorphism at the base number position 3932 of the apolipoprotein E gene.

12. A kit for detecting the genotype, comprising two or more of nucleic acids selected from the group consisting of the following (18) to (22):

(18) a nucleic acid for analyzing polymorphism at the base number position -668 of the plasminogen activator inhibitor-1 gene;

(19) a nucleic acid for analyzing polymorphism at the base number position -482 of the apolipoprotein C-III gene;

(20) a nucleic acid for analyzing polymorphism at the base number position 584 of the paraoxonase gene;

(21) a nucleic acid for analyzing polymorphism at the base number position 1018 of the glycoprotein Ibα gene; and

(22) a nucleic acid for analyzing polymorphism at the base number position 3932 of the apolipoprotein E gene.

13. Fixed nucleic acids comprising the following two or more nucleic acid selected from the group consisting of the following (1) to (7) fixed to an insoluble support:

(1) a nucleic acid for analyzing polymorphism at the base number position 3932 of the apolipoprotein E gene;

(2) a nucleic acid for analyzing polymorphism at the base number position 1648 of the glycoprotein Ia gene;

(3) a nucleic acid for analyzing polymorphism at the base number position

-863 of the tumor necrosis factor-α gene;

(4) a nucleic acid for analyzing polymorphism at the base number position 825 of G-protein β3 subunit gene;

(5) a nucleic acid for analyzing polymorphism at the base number position -482 of the apolipoprotein C-III gene; and

(6) a nucleic acid for analyzing polymorphism at the base number position -6 of the angiotensinogen gene.

14. Fixed nucleic acids comprising the following two or more nucleic acid selected from the group consisting of the following (7) to (11) fixed to an insoluble support:

(7) a nucleic acid for analyzing polymorphism at the base number position 1186 of the thrombospondin 4 gene;

(8) a nucleic acid for analyzing polymorphism at the base number position -863 of the tumor necrosis factor-α gene;

(9) a nucleic acid for analyzing polymorphism at the base number position 2136 of the thrombomodulin gene;

(10) a nucleic acid for analyzing polymorphism at the base number position 5713 of the thrombopoietin gene; and

(11) a nucleic acid for analyzing polymorphism at the base number position 994 of the platelet-activating factor acetylhydrolase gene.

15. Fixed nucleic acids comprising the following two or more nucleic acid selected from the group consisting of the following (12) to (17) fixed to an insoluble support:

(12) a nucleic acid for analyzing polymorphism at the base number position 561 of the E-selectin gene;

(13) a nucleic acid for analyzing polymorphism at the base number position 2445 of the fatty acid-binding protein 2 gene;

(14) a nucleic acid for analyzing polymorphism at the base number position 1018 of glycoprotein Ibα gene;

(15) a nucleic acid for analyzing polymorphism at the base number position -668 of the plasminogen activator inhibitor-1 gene;

(16) a nucleic acid for analyzing polymorphism at the base number position 584 of the paraoxonase gene; and

(17) a nucleic acid for analyzing polymorphism at the base number position 3932 of the apolipoprotein E gene.

16. Fixed nucleic acids comprising the following two or more nucleic acid selected from the group consisting of the following (18) to (22) fixed to an insoluble support:

(18) a nucleic acid for analyzing polymorphism at the base number position -668 of the plasminogen activator inhibitor-1 gene;

(19) a nucleic acid for analyzing polymorphism at the base number position -482 of the apolipoprotein C-III gene;

(20) a nucleic acid for analyzing polymorphism at the base number position 584 of the paraoxonase gene;

(21) a nucleic acid for analyzing polymorphism at the base number position 1018 of the glycoprotein Ibα gene; and

(22) a nucleic acid for analyzing polymorphism at the base number position 3932 of the apolipoprotein E gene.